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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2011; month=5; day=26; hr=9; min=25; sec=43; ms=934;]

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Application No: 10572740 Version No: 1.0

Input Set:**Output Set:**

Started: 2011-05-26 09:10:17.473
Finished: 2011-05-26 09:10:35.518
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 45 ms
Total Warnings: 409
Total Errors: 0
No. of SeqIDs Defined: 409
Actual SeqID Count: 409

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2011-05-26 09:10:17.473
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Error code

Error Description

This error has occurred more than 20 times, will not be displayed

<110> APPLICANT: Micromet AG
<120> TITLE OF INVENTION: Multispecific deimmunized CD3 binders
<130> FILE REFERENCE: G 2728 PCT

<140> CURRENT APPLICATION NUMBER:10572740
<141> CURRENT FILING DATE:2011-05-26
<160> NUMBER OF SEQ ID NOS: 409
<170> SOFTWARE: PatentIn version 3.1

<210> SEQ ID NO 1
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: wt Anti-CD3 cassette

<400> SEQUENCE: 1
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tcctgcaaga cttctggcta cacctttact aggtacacga tgcactgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac 240
atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca ctctcacagt ctctcagtc 360
gaaggtggaa gtggagggttc tgggtggaagt ggagggttcag gtggagtcga cgacattcag 420
ctgaccagtc ctccagcaat catgtctgca tctccagggg agaaggtcac catgacctgc 480
agagccagtt caagtgtgaa ttacatgaac tgggtaccagc agaagtcagg cacctcccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tcccttatcg cttcagtggc 600
agtgggtctg ggacctcata ctctctcaca atcagcagca tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtgctgg gaccaagctg 720
gagctgaaa 729

<210> SEQ ID NO 2
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: wt Anti-CD3 cassette

<400> SEQUENCE: 2
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Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly
115 120 125
Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser
130 135 140
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
165 170 175
Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190
Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
195 200 205
Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
225 230 235 240
Glu Leu Lys

<210> SEQ ID NO 3
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: deimmunized linker
<400> SEQUENCE: 3
Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
1 5 10 15
Ala Asp

<210> SEQ ID NO 4
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH2/VL1
<400> SEQUENCE: 4
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tcctgcaagg cttctggcta caccgctact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaatacta gccgtgggta tactaattac 180
gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtacta gtactggttc tgggtggaagt ggagggttcag gtggagcaga cgacattcag 420
atgaccagtc ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
agagccagtc aaagtgtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tcctgtctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
gagatcaaa 729

<210> SEQ ID NO 5
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH2/VL1
<400> SEQUENCE: 5
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50 55 60
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160
Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205
Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240
Glu Ile Lys

<210> SEQ ID NO 6
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH2/VL2
<400> SEQUENCE: 6
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tcctgcaagg cttctggcta caccgtact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
gaaggtacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaaggtg 720
gagatcaaa 729

<210> SEQ ID NO 7
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH2/VL2
<400> SEQUENCE: 7
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr

	20		25		30										
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
	35		40		45										
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Ala	Gln	Lys	Leu
	50		55		60										
Gln	Gly	Arg	Val	Thr	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr
65			70		75									80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys
			85		90									95	
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly
	100		105		110										
Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Glu	Gly	Thr	Ser	Thr	Gly	Ser	Gly
	115		120		125										
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ala	Asp	Asp	Ile	Val	Leu	Thr	Gln	Ser
	130		135		140										
Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys
145			150		155									160	
Arg	Ala	Ser	Gln	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro
			165		170									175	
Gly	Lys	Ala	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser
	180		185		190										
Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser
	195		200		205										
Leu	Thr	Ile	Asn	Ser	Leu	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
	210		215		220										
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val
225			230		235									240	
Glu	Ile	Lys													

<210> SEQ ID NO 8
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH2/VL3
<400> SEQUENCE: 8

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tcttgcaagg	cttctggcta	caccgctact	aggtacacga	tgcactgggt	aaggcaggca	120
cctggacagg	gtctggaatg	gattggatac	attaatccta	gccgtggtta	tactaattac	180
gcacagaagt	tgcagggccg	cgtcacaatg	actacagaca	cttccaccag	cacagcctac	240
atggaactga	gcagcctgcg	ttctgaggac	actgcaacct	attactgtgc	aagatattat	300
gatgatcatt	actgccttga	ctactggggc	caaggcacca	cggtcaccgt	ctcctcaggc	360
gaaggtacta	gtactggttc	tgggtggaagt	ggaggttcag	gtggagcaga	cgacattgta	420
ctgacccagt	ctccagcaac	tctgtctctg	tctccagggg	agcgtgccac	cctgacctgc	480
agagccagtt	caagtgtaag	ttacatgaac	tggtaccagc	agaagccggg	caaggcaccc	540
aaaagatgga	tttatgacac	atccaaagtg	gcttctggag	tccctgctcg	cttcagtggc	600
agtgggtctg	ggaccgacta	ctctctcaca	atcaacagct	tggaggctga	agatgctgcc	660
acttattact	gccaacagtg	gagtagtaac	ccgctcacgt	tcggtggcgg	gaccaagggtg	720
gagatcaaa						729

<210> SEQ ID NO 9
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH2VL3
<400> SEQUENCE: 9

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50 55 60
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160
Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205
Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240
Glu Ile Lys

<210> SEQ ID NO 10
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH3/VL1
<400> SEQUENCE: 10
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cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180
gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
ctgcaaataga acagcctgaa aactgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
gaaggtaacta gtactggttc tgggtggaagt ggagggttcag gtggagcaga cgacattcag 420
atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
gagatcaaa 729

<210> SEQ ID NO 11
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: artificial sequence

<220> FEATURE:
<223> OTHER INFORMATION: VH3/VL1
<400> SEQUENCE: 11
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50 55 60
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160
Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205
Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240
Glu Ile Lys

<210> SEQ ID NO 12
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH3/VL2
<400> SEQUENCE: 12
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cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180
gcacagaag